Ellen M Schmidt

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

22 papers	8,042 citations	18 h-index	26 g-index
26 ext. papers	10,777 ext. citations	24.9 avg, IF	3.84 L-index

#	Paper	IF	Citations
22	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
21	Discovery and refinement of loci associated with lipid levels. *Nature Genetics*, **2013**, 45, 1274-1283	36.3	1904
20	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
19	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. *Nature Genetics*, **2018**, 50, 1505-1513	36.3	675
18	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
17	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. *Nature Genetics*, **2018**, 50, 1234-1239	36.3	254
16	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. *Nature Genetics*, **2016**, 48, 1171-1184	36.3	251
15	Systematic evaluation of coding variation identifies a candidate causal variant in TM6SF2 influencing total cholesterol and myocardial infarction risk. *Nature Genetics*, **2014**, 46, 345-51	36.3	213
14	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. *Nature Communications*, **2016**, 7, 10495	17.4	180
13	Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. *American Journal of Human Genetics*, **2014**, 94, 233-45	11	170
12	GREGOR: evaluating global enrichment of trait-associated variants in epigenomic features using a systematic, data-driven approach. *Bioinformatics*, **2015**, 31, 2601-6	7.2	96
11	Association of Polygenic Risk Scores for Multiple Cancers in a Phenome-wide Study: Results from The Michigan Genomics Initiative. *American Journal of Human Genetics*, **2018**, 102, 1048-1061	11	83
10	A Fast and Accurate Algorithm to Test for Binary Phenotypes and Its Application to PheWAS. *American Journal of Human Genetics*, **2017**, 101, 37-49	11	66
9	Genome-wide association study of delay discounting in 23,217 adult research participants of European ancestry. *Nature Neuroscience*, **2018**, 21, 16-18	25.5	56
8	Genome-wide Study of Atrial Fibrillation Identifies Seven Risk Loci and Highlights Biological Pathways and Regulatory Elements Involved in Cardiac Development. *American Journal of Human Genetics*, **2018**, 102, 103-115	11	53
7	Exploring and visualizing large-scale genetic associations by using PheWeb. *Nature Genetics*, **2020**, 52, 550-552	36.3	41
6	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24

List of Publications

5	Chromosome 1q21.2 and additional loci influence risk of spontaneous coronary artery dissection and myocardial infarction. *Nature Communications*, **2020**, 11, 4432	17.4	22
4	No large-effect low-frequency coding variation found for myocardial infarction. *Human Molecular Genetics*, **2014**, 23, 4721-8	5.6	14
3	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. *Nature Genetics*, **2022**,	36.3	7
2	LabWAS: Novel findings and study design recommendations from a meta-analysis of clinical labs in two independent biobanks. *PLoS Genetics*, **2020**, 16, e1009077	6	6
1	Insights into blood lipids from rare variant discovery. *Current Opinion in Genetics and Development*, **2015**, 33, 25-31	4.9	4